SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gately, Maurice K.
Presky, David H.

(ii) TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-12

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Hoffmann-La Roche Inc.
(B) STREET: 340 Kingsland Street
(C) CITY: Nutley
(D) STATE: New Jersey
(E) COUNTRY: United States
(F) ZIP: 07110-1199

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Buchholz, Briana C.
(B) REGISTRATION NUMBER: 39,123
(C) REFERENCE/DOCKET NUMBER: CD 1048P

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 973-235-6208
(B) TELEFAX: 973-235-2363

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: mouse
(G) CELL TYPE: Hybridoma
(H) CELL LINE: HIL-12F3-16G2

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CTG GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC
48
Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser
 1               5                  10                  15

CTC ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC
96
Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn
            20                  25                  30

TGG ATC CGG AAA TTC CCA GGG AAT AAA TTT GAG TAC ATG GGA TTC ATA
144
Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile
        35                  40                  45

AGT TAT AGT GGT AGC ACT TAC AAT AAT CCA TCT CTC AAA AAT CGA GTC
192
Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val
    50                  55                  60

TCC ATC ACT CGA GAC ACA TCC AAT AAC CAG TAC TAC CTG CAG TTG AGT
240
Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser
65                  70                  75                  80

TCT GTG ACT ACT GAG GAC TCA GCC ACA TAT TAC TGT GCA AGA TCT TCG
288
Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser
                85                  90                  95

GAT GCT TTG GAC TAC TGG GGC GCA GGG ACC ACG
321
Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser
 1               5                  10                  15

Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn
            20                  25                  30

Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile
        35                  40                  45

Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val
    50                  55                  60

Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser
65                  70                  75                  80

Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser
                85                  90                  95

Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: mouse
(G) CELL TYPE: Hybridoma

(H) CELL LINE: HIL-12F3-20E11

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC CTC
48
Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu
1 5 10 15

ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC TGG
96
Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp
20 25 30

ATC CGG AAA TTC CCA GAT AAT ACA CTT GAG TAC ATG GGA TAC ATA AGT
144
Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser
35 40 45

TAC AGT GGT AGT ACT TAC TAC AAT CCA TCT CTC AGA AGT CGA ATC TCC
192
Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser
50 55 60

ATC ACT CGA GAC ACA TCC AAG AAC CAG TAC TCC ATG CAG TTG AAT TCT
240
Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser
65 70 75 80

GTG ACT ACT GAG GAC ACA GCC ACA TAT TAC TGT GCA AGA TCC TCG GAT
288
Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp
85 90 95

GCT ATG GAC TAC TGG GGC GC
308
Ala Met Asp Tyr Trp Gly
100

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu
1 5 10 15

Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp
20 25 30

Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser
35 40 45

Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser
50 55 60

Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser
65 70 75 80

Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp
85 90 95

Ala Met Asp Tyr Trp Gly
100